

Please amend claim 33 as follows:

- 33 [Amended]. The method of claim [31] 47, wherein [in step (D),] said amplification [interrogation] is accomplished using [a] nucleic acid primers [molecule] having a nucleotide sequence that specifically hybridizes to an invariant proximal or invariant/distal nucleotide sequence of [a] each single nucleotide polymorphism present in said DNA molecule of [a] said target human[, wherein said genetic bit analysis permits specific detection of the single nucleotide polymorphic site (X) of said single nucleotide polymorphism]. --

[Please amend claim 34 as follows:]

- 34 [Amended]. The method of claim [31] 47, wherein said method additionally includes the steps:
- (E) comparing each of said [interrogated] identified single nucleotide polymorphisms of said target human, with a corresponding single nucleotide polymorphism of a reference human, and determining whether said polymorphisms contain the same single nucleotide at their respective polymorphic sites; and
- (F) using said comparison to determine the extent of genetic similarity between said target human and said reference human. --

[Please amend claim 35 as follows:]

- 35 [Twice Amended]. The method of claim [31] 34, wherein in step (F), said determination is sufficient to establish that said target human and said reference human are not the same person. --

[Please amend claim 36 as follows:]

- 36 [Twice Amended]. The method of claim [31] 34, wherein in step (F), said determination is sufficient to establish that said reference human is not a parent of said target human. --

[Please amend claim 37 as follows:]

- 37 [Twice Amended]. The method of claim [31] 34, wherein said reference human has a trait, and said determination of step (F) is sufficient to establish that said target human also has said trait. --

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concluded

[Please amend claim 38 as follows:]

- 38 [Twice Amended]. The method of claim [31] 34, wherein said reference human has a first and second trait, and said determination of step (F) is sufficient to establish a genetic linkage between said traits. --

Please add the following new claims:

- 47. A method for analyzing DNA of a target human by identifying at least two single nucleotide polymorphic sites, wherein said method comprises:
- (A) selecting said at least two single nucleotide polymorphic sites for such analysis;
 - (B) amplifying DNA of said target human containing each of said polymorphic sites;
 - (C) determining the identity of the single nucleotide present at each of said single nucleotide polymorphic sites; and
 - (D) comparing the identity of said determined single nucleotide present at each of said single nucleotide polymorphic sites with the identity of a reference nucleotide, said reference nucleotide being present at each of said single nucleotide polymorphic sites in a reference organism.
48. The method of claim 47, wherein said method additionally comprises identifying the presence of a genetic trait of said target human, and wherein at least one of said single nucleotide polymorphic sites is within about 150 bases of said genetic trait.
49. A method for determining whether a target human possesses a genetic trait, said method comprising the steps:
- (A) amplifying a DNA molecule of said human, wherein said DNA molecule contains at least one single nucleotide polymorphism and wherein said single nucleotide polymorphism is within about 150 bases of said genetic trait;
 - (B) incubating the DNA of said human in the presence of a nucleic acid primer and from one to four dideoxynucleotide derivatives, under conditions sufficient to permit a polymerase mediated, template-dependent extension of said primer, said extension causing the incorporation of a single dideoxynucleotide derivative to the 3'-terminus of said primer, said incorporated single dideoxynucleotide derivative